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(FILE 'HOME' ENTERED AT 09:32:43 ON 31 MAY 2006)

FILE 'AGRICOLA, MEDLINE, CAPLUS, BIOSIS' ENTERED AT 09:32:46 ON 31 MAY 2006

L1 10280 S RHODOCOCCLUS
L2 234 S L1 (10N) DEHYDROGENASE
L3 156 DUP REM L2 (78 DUPLICATES REMOVED)
L4 67 S L3 AND ALCOHOL
L5 40 S L4 AND PY<2003
L6 2 S L5 AND RUBER

FILE 'STNGUIDE' ENTERED AT 09:35:04 ON 31 MAY 2006

FILE 'AGRICOLA, MEDLINE, CAPLUS, BIOSIS' ENTERED AT 09:43:15 ON 31 MAY 2006

L7 12 S L3 AND RUBER
L8 12 DUP REM L7 (0 DUPLICATES REMOVED)
L9 113 S L3 AND PY<2003
L10 4 S L8 AND PY<2003

FILE 'STNGUIDE' ENTERED AT 09:48:34 ON 31 MAY 2006

FILE 'AGRICOLA, MEDLINE, CAPLUS, BIOSIS' ENTERED AT 09:49:25 ON 31 MAY 2006



FILE 'STNGUIDE' ENTERED AT 09:50:31 ON 31 MAY 2006

FILE 'AGRICOLA, MEDLINE, CAPLUS, BIOSIS' ENTERED AT 09:52:39 ON 31 MAY 2006

L11 10 S L5 AND (STERO? OR KDA OR DA OR ZN)
L12 17 S L5 AND (STER? OR OPTI? OR KDA OR DA OR ZN)

FILE 'STNGUIDE' ENTERED AT 09:55:13 ON 31 MAY 2006

	Type	L #	Hits	Search Text
1	BRS	L1	2856	rhodococcus
2	BRS	L2	235	l1 and (alcohol near2 dehydrogenase)
3	BRS	L3	29	l2 and ruber
4	BRS	L4	26	l2 and (rhodococcus near2 ruber)
5	BRS	L5	2	(alcohol near2 dehydrogenase) near10 (rhodococcus near2 ruber)
6	BRS	L6	16	(alcohol near2 dehydrogenase) near10 (rhodococcus)

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project

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Clusters of orthologous
groups

Protein reviews on the
web

Search for full length
cDNAs

- Search History will be lost after eight hours of inactivity.
- To combine searches use # before search number, e.g., #2 AND #6.
- Search numbers may not be continuous; all searches are represented.
- Click on query # to add to strategy

Search	Most Recent Queries	Time	Result
#17	Search txid1830[Organism:noexp] AND dehydrogenase	12:33:03	14
#16	Search txid1830[Organism:noexp]	12:32:59	58
#13	Protein Links for PubMed (Select 10531651)	12:31:11	2

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May 22 2006 06:31:57

RESULT 1

US-10-004-115B-34

; Sequence 34, Application US/10004115B

; Patent No. 6884607

; GENERAL INFORMATION:

; APPLICANT: ASAKO, HIROYUKI

; APPLICANT: MATSUMURA, KENJI

; APPLICANT: SHIMIZU, MASATOSHI

; APPLICANT: ITO, NOBUYA

; APPLICANT: WAKITA, RYUHEI

; TITLE OF INVENTION: PROCESS FOR PRODUCING OPTICALLY ACTIVE

; TITLE OF INVENTION: 4-HALO-3-HYDROXYBUTANOATE

; FILE REFERENCE: 7372-72249

; CURRENT APPLICATION NUMBER: US/10/004,115B

; CURRENT FILING DATE: 2001-12-06

; PRIOR APPLICATION NUMBER: JP 2000-372704

; PRIOR FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: JP 2001-006144

; PRIOR FILING DATE: 2001-01-15

; PRIOR APPLICATION NUMBER: JP 2001-026594

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: JP 2001-175175

; PRIOR FILING DATE: 2001-06-11

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 34

; LENGTH: 348

; TYPE: PRT

; ORGANISM: Corynebacterium sp.

US-10-004-115B-34

Query Match 64.9%; Score 1152.5; DB 2; Length 348;

Best Local Similarity 63.6%; Pred. No. 1.8e-101;

Matches 220; Conservative 40; Mismatches 85; Indels 1; Gaps 1;

```

Qy      1 MKAVQYTEIGSEPVVVDIPTPTPGPGEILLKVTAAGLCHSDIFVMDMPAAQYAYGLPLTL 60
      |||:| | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MKAIQYTRIGAEPELTEIPKPEPGPGEVLLVTAAGVCHSDDFIMSLPEEQYTYGLPLTL 60

Qy     61 GHEGVGTVAELGEGVTGFGVGDAVAVYGPWGCACHACARGRENYCTRAADLGITPPGLG 120
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     61 GHEGAGKVAAVGEGVEGLDIGTNVVVYGPWGCNCWHCSQGLENYCSRAQELGINPPGLG 120

Qy    121 SPGSMAEYMIVDSARHLVPIGDLDPVAAAPLTDAGLTPYHAISRVLPLLPGPGSTAVVIGV 180
      : | | : | | : | | | | | | | | | | | | | | | | | | | | | |
Db    121 APGALAEFMIVDSPRHLVPIGDLDPVKTVPLTDAGLTPYHAIKRSLPKLRGGSYAVVIGT 180

Qy    181 GGLGHVGIQILRAVSAARVIAVDLDDRLALAREVGADA AVKSGAGAADAIRELTGGQGA 240
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    181 GGLGHVAIQLLRHLAATVIALDVSADKLELATKVGAEVVLSDKDAENVRKITGSQGA 240

Qy    241 TAVFDFVGAQSTIDTAQQVAVDGHISVVGIIHAG-AHAKVGFFMIPFGASVVTPTYWGTRS 299
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    241 ALVLDVFGYQPTIDTAMAVAGVGS DVTIVGIGDQGAHAKVGFFQSPYEASVTVPYWGARN 300

Qy    300 ELMEVVALARAGRLDIHTETFTLDEGPAAYRRLREGSIRGRGVVVP 345
      | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db    301 ELIELIDLAHAGIFDISVETFSLDNGAEAYRRLAAGTSLGRAVVVP 346

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      :||:|:|:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      121 APGALAEFMIVDSPRHLVPIGDLDPVKTVPLTDAGLTPYHAIKRSLPKLRGGSYAVVIGT 180
Qy      181 GGLGHVGIQILRAVSAARVIAVDLDDRLALAREVGADAAVKSGAGAADAIRELTTGGQGA 240
      ||||| ||:| | :||| |||:|: | :| || :||| | | ||: |:|:| | |||
Db      181 GGLGHVAIQLLRHLAATVIALDVSADKLELATKVGAEVVLSDKDAAENVRKITGSQGA 240
Qy      241 TAVFDFVGAQSTIDTAQQVVAVDGHISVVGIHAG-AHAKVGFFMIPFGASVVTPYWGTRS 299
      | |||| | |||| | | :|:| | | ||||| | :| || |||| |:
Db      241 ALVLDFVGYQPTIDTAMAVAGVGS DVTIVGIGDQAHAKVGFFQSPYEASVTVPYWGARN 300
Qy      300 ELMEVVALARAGRLDIHTETFTLDEGPAAYRRLREGSIRGRGVVVP 345
      ||:|:| | | || | |||:| | | |||| |:| | ||||
Db      301 ELIELIDLAHAGIFDISVETFSLDNGAEAYRRLAAGTSLGRAVVVP 346

```

RESULT 1

US-09-252-991A-26632

; Sequence 26632, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 26632

; LENGTH: 233

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-26632

Query Match 90.7%; Score 39; DB 2; Length 233;

Best Local Similarity 80.0%; Pred. No. 17;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGAGAADAXR 10

:|||||||

Db 18 AGAGAADARR 27

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	35	81.4	123	2	H81235	50S ribosomal prot
2	34	79.1	255	2	JC7264	CCAAT-enhancer bin
3	34	79.1	263	2	B75361	WD-repeat family p
4	34	79.1	525	2	AF3274	hypothetical prote
5	34	79.1	547	1	S51475	cytochrome P450 cy
6	34	79.1	602	2	H87503	phosphogluconate d
7	34	79.1	741	2	D75500	ATP-dependent Clp
8	34	79.1	1335	2	H75511	DNA polymerase III
9	33	76.7	299	2	F75295	hypothetical prote
10	33	76.7	370	2	A60089	transforming prote
11	33	76.7	397	2	T35609	whiE protein I - S
12	33	76.7	428	2	S17817	bacteriochlorophyl
13	33	76.7	461	2	T51030	probable acetylorn
14	33	76.7	463	2	T34841	probable bifunctio
15	33	76.7	588	2	AC0611	transport ATP-bind
16	33	76.7	588	2	B85614	hypothetical prote
17	33	76.7	588	2	D90750	hypothetical prote
18	33	76.7	588	2	F64827	ABC-type

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	42	97.7	346	2	Q8KLT9_9NOCA	Q8klt9 rhodococcus
2	39	90.7	478	2	Q82F52_STRAW	Q82f52 streptomyce
3	38	88.4	557	2	Q2T4A0_BURTH	Q2t4a0 burkholderi
4	38	88.4	581	2	Q5KGT5_CRYNE	Q5kgt5 cryptococcu
5	38	88.4	613	2	Q55SE1_CRYNE	Q55se1 cryptococcu
6	38	88.4	964	2	Q4KXA8_LEIME	Q4kxa8 leishmania
7	37	86.0	737	2	Q8LTQ2_9CAUD	Q8ltq2 lactococcus
8	36	83.7	241	2	Q651U8_ORYSA	Q65lu8 oryza sativ
9	36	83.7	248	2	Q84R34_ORYSA	Q84r34 oryza sativ
10	36	83.7	379	2	Q3GCC8_9FIRM	Q3gcc8 syntrophomo
11	35	81.4	73	2	Q7R475_GIALA	Q7r475 giardia lam
12	35	81.4	81	2	Q341E1_RHOPA	Q341e1 rhodopseudo
13	35	81.4	122	1	RL7_NEIMA	P0a0x0 neisseria m
14	35	81.4	122	1	RL7_NEIMB	P0a0x1 neisseria m
15	35	81.4	123	2	Q5F5R4_NEIG1	Q5f5r4 neisseria g
16	35	81.4	132	2	Q4DER8_TRYCR	Q4der8 trypanosoma
17	35	81.4	135	2	Q4D9Q6_TRYCR	Q4d9q6 trypanosoma
18	35	81.4	296	2	P72540_STRPR	

RESULT 1

Q8KLT9_9NOCA

ID Q8KLT9_9NOCA PRELIMINARY; PRT; 346 AA.

AC Q8KLT9;

DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2002, sequence version 1.

DT 07-FEB-2006, entry version 19.

DE Secondary alcohol dehydrogenase (EC 1.1.1.1).

GN Name=sadh;

OS Rhodococcus ruber.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Nocardiaceae; Rhodococcus.

OX NCBI_TaxID=1830;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=219;

RA Tamak C., Plattner H., Hummel W., Diekmann H., Meens J.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

CC -!- COFACTOR: Zinc (By similarity).

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 CC -----

DR EMBL; AJ491307; CAD36475.1; -; Genomic_DNA.

DR HSSP; Q59096; 1F8F.

DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.

DR GO; GO:0046872; F:metal ion binding; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR InterPro; IPR013154; ADH_N.

DR InterPro; IPR002085; ADH_Sf_Zn.

DR InterPro; IPR002328; ADH_Zn.

DR InterPro; IPR013149; ADH_Zn_bd.

DR InterPro; IPR002110; ANK.

DR PANTHER; PTHR11695; Adh_zn_family; 1.

DR PRINTS; PR01415; ANKYRIN.

DR PROSITE; PS00059; ADH_ZINC; 1.

KW Metal-binding; NAD; Oxidoreductase; Zinc.

SQ SEQUENCE 346 AA; 35449 MW; F885D8B0F7E6C1CC CRC64;

Query Match 97.7%; Score 42; DB 2; Length 346;

Best Local Similarity 90.0%; Pred. No. 27;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGAGAADAXR 10

|||||||

Db 223 SGAGAADAIR 232

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1775	100.0	345	9	ADY85204	Ady85204 Rhodococc
2	1188.5	67.0	346	9	ADZ03703	Adz03703 Streptomy
3	1152.5	64.9	348	8	ADL18256	Adl18256 Corynebac
4	1152.5	64.9	348	9	ADV69575	Adv69575 Corynebac
5	1151.5	64.9	348	7	ADF53768	Adf53768 Alcohol d
6	1150.5	64.8	348	9	AED84856	Aed84856 Alcohol d
7	1145.5	64.5	348	9	AED84855	Aed84855 Alcohol d
8	1100.5	62.0	344	8	ADN25583	Adn25583 Bacterial
9	1061.5	59.8	384	8	ADK70245	Adk70245 Corynebac
10	1061.5	59.8	385	5	AAO21525	Aao21525 385-mer C
11	1061.5	59.8	385	5	ABB77974	Abb77974 Amino aci
12	1061.5	59.8	385	7	ADE39627	Ade39627 Corynebac
13	1061.5	59.8	385	8	ADF88657	Adf88657 3-quinucl
14	1061.5	59.8	385	8	ADK82546	Adk82546 Isomerase
15	1061.5	59.8	385	8	ADM46684	Adm46684 385 amino
16	1061.5	59.8	385	8	ADM46565	Adm46565 Corynebac
17	916.5	51.6	327	8	ADN25512	Adn25512 Bacterial
18	577	32.5	162	9	AED84825	Aed84825 Alcohol d
19	559	31.5	161	9	AED84826	Aed84826 Alcohol d
20	556	31.3	162	9	AED84823	Aed84823 Alcohol d
21	533	30.0	341	9	ADZ47402	Adz47402 341 amino
22	480.5	27.1	359	8	ADS44521	Ads44521 Bacterial
23	476	26.8	128	9	AED84824	

Database : Issued_Patents_AA:*
 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1152.5	64.9	348	2	US-10-004-115B-34	Sequence 34, Appl
2	1061.5	59.8	385	2	US-09-984-334-1	Sequence 1, Appli
3	481.5	27.1	352	2	US-09-504-358-18	Sequence 18, Appl
4	481.5	27.1	352	2	US-09-954-314-18	Sequence 18, Appl
5	481.5	27.1	352	2	US-10-230-562-18	Sequence 18, Appl
6	465.5	26.2	352	2	US-09-648-004-24	Sequence 24, Appl
7	465.5	26.2	352	2	US-10-272-419-24	Sequence 24, Appl
8	463.5	26.1	381	2	US-09-248-796A-20906	Sequence 20906, A
9	422.5	23.8	336	1	US-08-713-254-2	Sequence 2, Appli
10	422.5	23.8	336	2	US-08-855-767-2	Sequence 2, Appli
11	414.5	23.4	346	2	US-09-489-039A-9885	Sequence 9885, Ap
12	403	22.7	344	2	US-09-134-001C-5343	Sequence 5343, Ap
13	394.5	22.2	465	2	US-09-252-991A-18919	Sequence 18919, A
14	374.5	21.1	375	2	US-09-134-000C-5937	Sequence

Database : Published_Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1775	100.0	345	4	US-10-666-205-48	Sequence 48, Appl
2	1713	96.5	346	6	US-11-087-099-9022	Sequence 9022, Ap
3	1152.5	64.9	348	5	US-10-617-034A-1	Sequence 1, Appli
4	1151.5	64.9	348	6	US-11-188-298-13982	Sequence 13982, A
5	1100.5	62.0	344	4	US-10-369-493-8236	Sequence 8236, Ap
6	1061.5	59.8	385	3	US-09-984-334-1	Sequence 1, Appli
7	1061.5	59.8	385	4	US-10-004-115A-34	Sequence 34, Appl
8	1061.5	59.8	385	4	US-10-327-108-1	Sequence 1, Appli
9	1061.5	59.8	385	5	US-10-920-239-34	Sequence 34, Appl
10	1061.5	59.8	385	6	US-11-087-099-1453	Sequence 1453, Ap
11	1061.5	59.8	385	6	US-11-188-298-1461	Sequence 1461, Ap
12	933.5	52.6	360	6	US-11-188-298-5305	Sequence 5305, Ap
13	916.5	51.6	327	4	US-10-369-493-8165	Sequence 8165, Ap
14	606	34.1	341	4	US-10-156-761-8932	Sequence

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	526	29.6	344	2	D90325	alcohol dehydrogen
2	480.5	27.1	359	2	C72533	probable alcohol d
3	472	26.6	347	1	S51120	alcohol dehydrogen
4	465	26.2	347	1	A44245	alcohol dehydrogen
5	455.5	25.7	349	2	B90285	alcohol dehydrogen
6	451.5	25.4	340	2	T37030	alcohol dehydrogen
7	445.5	25.1	236	2	T36399	probable alcohol d
8	442	24.9	346	2	H81915	probable alcohol d
9	442	24.9	348	2	H81186	probable alcohol d
10	419.5	23.6	336	2	AH0672	alcohol dehydrogen
11	419	23.6	365	2	T36806	probable alcohol d
12	417.5	23.5	342	2	H97434	alcohol dehydrogen
13	417.5	23.5	342	2	AD2653	alcohol dehydrogen
14	415	23.4	346	1	A64901	alcohol dehydrogen
15	415	23.4	346	2	G85728	alcohol dehydrogen

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1713	96.5	346	2	Q8KLT9_9NOCA	Q8klt9 rhodococcus
2	1188.5	67.0	346	2	Q9S5E6_STRCO	Q9s5e6 streptomyce
3	1168.5	65.8	348	2	Q415U1_KINRA	Q415u1 kineococcus
4	1152.5	64.9	348	2	Q65YQ4_9NOCA	Q65yq4 rhodococcus
5	1151.5	64.9	348	2	Q6YBW1_RHOER	Q6ybw1 rhodococcus
6	1151.5	64.9	348	2	Q9ZN85_9NOCA	Q9zn85 rhodococcus
7	1150.5	64.8	346	2	Q5YTY4_NOCFA	Q5yty4 nocardia fa
8	1100.5	62.0	348	2	Q47L68_THEFY	Q47l68 thermobifid
9	933.5	52.6	360	2	Q47PU4_THEFY	Q47pu4 thermobifid
10	881	49.6	343	2	Q46N63_RALEJ	Q46n63 ralstonia e
11	856.5	48.3	354	2	Q3H4C5_9ACTO	Q3h4c5 nocardioide
12	742.5	41.8	347	2	Q5YR32_NOCFA	Q5yr32 nocardia fa
13	704	39.7	359	2	Q5YXH9_NOCFA	Q5yxh9 nocardia fa
14	606	34.1	341	2	Q82NB0_STRAW	Q82nb0 streptomyce
15	579	32.6	347	2	Q3X235_9ACTN	Q3x235 rubrobacter
16	566	31.9	341	2	Q4J706_SULAC	Q4j706 sulfolobus
17	555.5	31.3	353	2	Q3WYQ7_9ACTN	Q3wyq7 rubrobacter
18	553	31.2	341	2	Q8CK64_STRCO	Q8ck64 streptomyce
19	552	31.1	341	2	Q2JA11_9ACTO	Q2ja11 frankia

RESULT 1

Q8KLT9_9NOCA

ID Q8KLT9_9NOCA PRELIMINARY; PRT; 346 AA.

AC Q8KLT9;

DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2002, sequence version 1.

DT 07-FEB-2006, entry version 19.

DE Secondary alcohol dehydrogenase (EC 1.1.1.1).

GN Name=sadh;

OS Rhodococcus ruber.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Nocardiaceae; Rhodococcus.

OX NCBI_TaxID=1830;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=219;

RA Tamak C., Plattner H., Hummel W., Diekmann H., Meens J.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

CC -!- COFACTOR: Zinc (By similarity).

CC

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CC

DR EMBL; AJ491307; CAD36475.1; -; Genomic_DNA.

DR HSSP; Q59096; 1F8F.

DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.

DR GO; GO:0046872; F:metal ion binding; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR InterPro; IPR013154; ADH_N.

DR InterPro; IPR002085; ADH_Sf_Zn.

DR InterPro; IPR002328; ADH_Zn.

DR InterPro; IPR013149; ADH_Zn_bd.

DR InterPro; IPR002110; ANK.

DR PANTHER; PTHR11695; Adh_zn_family; 1.

DR PRINTS; PR01415; ANKYRIN.

DR PROSITE; PS00059; ADH_ZINC; 1.

KW Metal-binding; NAD; Oxidoreductase; Zinc.

SQ SEQUENCE 346 AA; 35449 MW; F885D8B0F7E6C1CC CRC64;

Query Match 96.5%; Score 1713; DB 2; Length 346;

Best Local Similarity 95.7%; Pred. No. 8.1e-102;

Matches 330; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

```

Qy      1 MKAVQYTEIGSEPVVVDIPTPTPGPEILLKVTAAGLCHSDIFVMDMPAAQYAYGLPLTL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MKALQYTEIGSEPVVVDVPTPAPGPGEILLKVTAAGLCHSDIFVMDMPAEQYIYGLPLTL 60

Qy      61 GHEGVGTVAELGEGVTGFGVGDAVAVYGPWGC GACHACARGRENYCTRAADLGITPPGLG 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 GHEGVGTVAELGAGVTGFETGDAVAVYGPWGC GACHACARGRENYCTRAAELGITPPGLG 120

Qy      121 SPGSMAEYMIVDSARHLVPIGDLDPVAAAPLTDAGLTPYHAISRVLPLLGP GSTAVVIGV 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      121 SPGSMAEYMIVDSARHLVPIGDLDPVAAVPLTDAGLTPYHAISRVLPLLGP GSTAVVIGV 180

Qy      181 GGLGHVGIQILRAVSAARVIAVDLDDRLALAREVGADAAVKSGAGAADAIRELTGGQGA 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      181 GGLGHVGIQILRAVSAARVIAVDLDDRLALAREVGADAAVKSGAGAADAIRELTGGEGA 240

Qy      241 TAVFDFVGAQSTIDTAQQVVAVDGHISVVG IHAGAHAKVGFFMIPFGASVVTPYWGTRSE 300

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Db	241	:	TAVFDFVGAQSTIDTAQQVVAIDGHISVVGIHAGAHAKVGFFMIPFGASVVTPYWGTRSE	300
Qy	301		LMEVVALARAGRLDIHTETFTLDEGPAAYRRLREGSIRGRGVVVP	345
Db	301	:	LMDVVDLARAGRLDIHTETFTLDEGPTAYRRLREGSIRGRGVVVP	345

RESULT 4

Q65YQ4_9NOCA

ID Q65YQ4_9NOCA PRELIMINARY; PRT; 348 AA.

AC Q65YQ4;

DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.

DT 25-OCT-2004, sequence version 1.

DT 07-FEB-2006, entry version 13.

DE Phenylacetaldehyde reductase.

GN Name=par;

OS Rhodococcus sp. ST-10.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Nocardiaceae; Rhodococcus.

OX NCBI_TaxID=85582;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ST-10;

RX PubMed=16085867; DOI=10.1128/AEM.71.8.4713-4720.2005;

RA Makino Y., Inoue K., Dairi T., Itoh N.;

RT "Engineering of Phenylacetaldehyde Reductase for Efficient Substrate

RT Conversion in Concentrated 2-Propanol.";

RL Appl. Environ. Microbiol. 71:4713-4720(2005).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ST-10;

RX MEDLINE=20000646; PubMed=10531651; DOI=10.1007/s002530051536;

RA Wang J., Sakakibara M., Liu J., Dairi T., Itoh N.;

RT "Cloning, sequence analysis, and expression in Escherichia coli of the

RT gene encoding phenylacetaldehyde reductases from styrene-assimilating

RT Corynebacterium sp. ST-10.";

RL Appl. Microbiol. Biotechnol. 52:386-392(1999).

CC -!- COFACTOR: Zinc (By similarity).

CC

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CC

DR EMBL; AB190261; BAD51480.1; -; Genomic_DNA.

DR GO; GO:0046872; F:metal ion binding; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR InterPro; IPR013154; ADH_N.

DR InterPro; IPR002085; ADH_Sf_Zn.

DR InterPro; IPR002328; ADH_Zn.

DR InterPro; IPR013149; ADH_Zn_bd.

DR PANTHER; PTHR11695; Adh_zn_family; 1.

DR PROSITE; PS00059; ADH_ZINC; 1.

KW Metal-binding; NAD; Oxidoreductase; Zinc.

SQ SEQUENCE 348 AA; 36222 MW; 57568097CF806BEB CRC64;

Query Match 64.9%; Score 1152.5; DB 2; Length 348;

Best Local Similarity 63.6%; Pred. No. 6.9e-66;

Matches 220; Conservative 40; Mismatches 85; Indels 1; Gaps 1;

QY 1 MKA VQY TEIGSEPVVVDIPTPTPGPG EILLKVTAAGLCHSDIFVMDMPAAQYAYGLPLTL 60

|||:|||| ||:|| : :|| | ||||:||||:||||:|||| | :| || |||||

Db 1 MKA IQY TRIGAEP ELTEIPKPEPGPG EVLLEVTAAGVCHSDDFIMSLPEEQYTYGLPLTL 60

QY 61 GHEGVGTVAELGEGVTGFGVGDAVAVYGPWGCGACHACARGRENYCTRAADLGITPPGLG 120

|||| | || :|||| | :| | ||||| | | :|| ||||:|| :||| |||||

Db 61 GHEGAGKVA AVGEGVEGLDIGTNVVVYGPWGCGNCWHCSQGLENYCSRAQELGINPPGLG 120

QY 121 SPGSMAEYMI VDSARHLVP IGDLPVAAAPLT DAGLTPYHAISRVLP LLGPGSTAVVIGV 180

Db	121	APGALAEFMIVDSPRHLVPIGDLDPVKTVPLTDAGLTPYHAIKRSLPKLRGGSYAVVIGT	180
Qy	181	GGLGHVGIQILRAVSAARVIAVDLDDRLALAREVGADAAVKSAGAGAADAIRELTGGQGA	240
Db	181	GGLGHVAIQLLRHLASAATVIALDVSADKLELATKVGAEHVVLSDKDAAENVRKITGSQGA	240
Qy	241	TAVFDFVGAQSTIDTAQQVVAVDGHISVVGIIHAG-AHAKVGFFMIPFGASVVTPTYWGTRS	299
Db	241	ALVLDFVGYQPTIDTAMAVAGVGS DVTIVGIGDGAHAKVGFFQSPYEASVTVPYWGARN	300
Qy	300	ELMEVVALARAGRLDIHTETFTLDEGPAAYRRLREGSIRGRGVVVP	345
Db	301	ELIELIDLAHAGIFDISVETFSLDNGAEAYRRLAAGTSLGRAVVVP	346

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	9	100.0	10	7	ADD44401	Add44401 Rhodococc
2	9	100.0	10	9	ADY85159	Ady85159 Rhodococc
3	8	88.9	248	8	ADX93553	Adx93553 Plant ful
4	8	88.9	267	8	ADX87812	Adx87812 Plant ful
5	8	88.9	268	8	ADX88645	Adx88645 Plant ful
6	8	88.9	345	9	ADY85204	Ady85204 Rhodococc
7	8	88.9	799	7	ABM88577	Abm88577 Rice abio
8	7	77.8	106	3	AAG26730	Aag26730 Zea mays
9	7	77.8	123	3	AAY81132	Aay81132 Neisseria
10	7	77.8	123	3	AAY81131	Aay81131 Neisseria
11	7	77.8	123	6	ABP80703	Abp80703 N. gonorr
12	7	77.8	123	6	ABU37479	Abu37479 Protein e
13	7	77.8	123	6	ABU37710	Abu37710 Protein e
14	7	77.8	123	8	ADP08183	Adp08183 Neisseria
15	7	77.8	137	3	AAG26729	Aag26729 Zea mays
16	7	77.8	137	8	ADQ09964	Adq09964 Borrelia
17	7	77.8	171	7	ABO71893	Abo71893 Pseudomon

Database : Issued_Patents_AA:*
 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7	77.8	171	2	US-09-252-991A-20639	Sequence 20639, A
2	7	77.8	233	2	US-09-252-991A-26632	Sequence 26632, A
3	7	77.8	298	2	US-09-252-991A-22985	Sequence 22985, A
4	7	77.8	414	2	US-09-252-991A-17165	Sequence 17165, A
5	7	77.8	485	2	US-09-252-991A-24868	Sequence 24868, A
6	7	77.8	614	2	US-09-252-991A-20210	Sequence 20210, A
7	7	77.8	717	2	US-09-252-991A-22029	Sequence 22029, A
8	7	77.8	743	2	US-09-252-991A-28327	Sequence 28327, A
9	6	66.7	118	2	US-08-301-162-10	Sequence 10, Appl
10	6	66.7	118	2	US-09-461-240-10	Sequence 10, Appl
11	6	66.7	118	2	US-09-968-927-10	Sequence 10, Appl
12	6	66.7	133	2	US-09-252-991A-30896	Sequence 30896, A
13	6	66.7	139	2	US-09-270-767-35479	Sequence 35479, A
14	6	66.7	139	2	US-09-270-767-50696	Sequence 50696, A
15	6	66.7	150	2	US-09-252-991A-29818	Sequence 29818, A
16	6	66.7	169	2	US-09-252-991A-26193	Sequence 26193, A

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	7	77.8	123	2	H81235	50S ribosomal prot
2	7	77.8	255	2	JC7264	CCAAT-enhancer bin
3	7	77.8	263	2	B75361	WD-repeat family p
4	6	66.7	109	1	R6BY11	acidic ribosomal p
5	6	66.7	112	2	B43601	LSR2 T-cell antige
6	6	66.7	137	2	AD3645	flagella basal bod
7	6	66.7	161	2	E70867	hypothetical prote
8	6	66.7	183	2	T51910	hypothetical prote
9	6	66.7	184	2	C95930	conserved hypothet

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	8	88.9	346	2	Q8KLT9_9NOCA	Q8klt9 rhodococcus
2	8	88.9	557	2	Q2T4A0_BURTH	Q2t4a0 burkholderi
3	8	88.9	581	2	Q5KGT5_CRYNE	Q5kgt5 cryptococcu
4	8	88.9	613	2	Q55SE1_CRYNE	Q55se1 cryptococcu
5	7	77.8	73	2	Q7R475_GIALA	Q7r475 giardia lam
6	7	77.8	98	2	Q7Y1Q2_MAIZE	Q7ylq2 zea mays (m
7	7	77.8	99	2	Q4P9Q4_USTMA	Q4p9q4 ustilago ma
8	7	77.8	122	1	RL7_NEIMA	P0a0x0 neisseria m
9	7	77.8	122	1	RL7_NEIMB	P0a0x1